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OM nucleic - nucleic search, using sw model

Run on: June 17, 2003, 11:16:48 ; Search time 2680.05 Seconds
(without alignments)
11304.265 Million cell updates/sec

Title: US-09-807-933B-12
Perfect score: 1041
Sequence: 1 atgaagtctccatcatgcg.....ctggttcgagcgcaagtaa 1041

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	241	23.2	919	6	A68072	A68072 Sequence 67
2	241	23.2	919	6	AR163168	AR163168 Sequence
3	236.6	22.7	1423	8	AR094309	AR094309 Sequence
4	235.2	22.6	1443	8	FSOKCH	L29381 Fusarium ox
5	235.2	22.6	1473	6	A21795	A21795 F. oxysporum
6	235.2	22.6	1473	6	A23637	A23637 F. oxysporu
7	235.2	22.6	1473	6	A23646	A23646 F. oxysporu
8	235.2	22.6	1473	6	A23955	A23955 Endoglucana
9	235.2	22.6	1473	6	A23959	A23959 Endoglucana
10	235.2	22.6	1473	6	A41660	A41660 Sequence 3
11	235.2	22.6	1473	6	AR072922	AR072922 Sequence
12	235.2	22.6	1473	6	BD002249	BD002249 Cellulase
13	235.2	22.6	1473	6	BD010853	BD010853 Cellulase
14	235.2	22.6	1473	6	I13885	I13885 Sequence 3
15	235.2	22.6	1473	6	I21317	I21317 Sequence 3
16	235.2	22.6	1473	6	I57984	I57984 Sequence 3
17	233.2	22.4	960	6	AR094305	AR094305 Sequence
18	231.8	22.3	927	6	AR094307	AR094307 Sequence
19	230.4	22.1	894	6	AR094306	AR094306 Sequence
20	228	21.9	1174	6	A92311	A92311 Sequence 1
21	228	21.9	1174	6	AR075389	AR075389 Sequence
22	228	21.9	1174	6	AR094310	AR094310 Sequence
23	224.6	21.6	922	6	A68078	A68078 Sequence 73
24	224.6	21.6	922	6	AR163171	AR163171 Sequence
25	222.8	21.4	924	6	A68074	A68074 Sequence 69
26	222.8	21.4	924	6	AR163169	AR163169 Sequence
27	221.4	21.3	785	3	AB045177	AB045177 Reticulit
28	217.2	20.9	1060	6	A21793	A21793 H. insolens
29	217.2	20.9	1060	6	A23635	A23635 H. insolens
30	217.2	20.9	1060	6	A23644	A23644 H. insolens
31	217.2	20.9	1060	6	A23953	A23953 Endoglucana
32	217.2	20.9	1060	6	A23957	A23957 Endoglucana
33	217.2	20.9	1060	6	A41658	A41658 Sequence 1
34	217.2	20.9	1060	6	A68060	A68060 Sequence 55
35	217.2	20.9	1060	6	AR059002	AR059002 Sequence
36	217.2	20.9	1060	6	AR072921	AR072921 Sequence
37	217.2	20.9	1060	6	AR163160	AR163160 Sequence
38	217.2	20.9	1060	6	BD010852	BD010852 Cellulase
39	217.2	20.9	1060	6	I13884	I13884 Sequence 1
40	217.2	20.9	1060	6	I21316	I21316 Sequence 1
41	217.2	20.9	1060	6	I57983	I57983 Sequence 1
42	216	20.7	840	3	AB045172	AB045172 Reticulit
43	215.4	20.7	710	3	AB045171	AB045171 Reticulit
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45	213.6	20.5	1132	6	AR094315	AR094315 Sequence

ALIGNMENTS

RESULT 1

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LOCUS	DEFINITION	Sequence 67 from Patent WO9743409.				
ACCESSION	A68072					
VERSION	A68072.1	GI:4756872				
KEYWORDS	unidentified.					
SOURCE	unidentified.					
ORGANISM	unclassified.					
REFERENCE	1 (bases 1 to 919)					
AUTHORS	Dalboege,H., Diderichsen,B., Sandal,T. and Kauppinen,S.					
TITLE	METHOD OF PROVIDING NOVEL DNA SEQUENCES					
JOURNAL	Patent: WO 9743409-A 67 20-NOV-1997;					
	NOVONORDISK AS (DK)					

KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 BASE COUNT
 ORIGIN

Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 919)
 Dalb.o slashed.ge.H., Sandal,T., Kauppinen,M.Sakari. and
 Diderichsen,Bslashedge.
 Method of providing a hybrid polypeptide exhibiting an activity of
 interest
 Patent: US 6270968-A 67 07-AUG-2001;
 Location/Qualifiers
 1. 919
 /organism="unknown"
 165 a 325 c 256 g 173 t

Query Match 23.2%; Score 241; DB 6; Length 919;
 Best Local Similarity 63.1%; Pred. No. 9.2e-35;
 Matches 392; Conservative 0; Mismatches 220; Indels 9; Gaps 1;

QY 417 TGGCTTCTCTGGAAACGGTCGCCTACTCCGCTACTCGGATTGCTGCAAGCCCTCTTTGCCG 476
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 QY 477 CTGGCAGGAAGGCTTCTGTAACTAAGCCTGTAFTCACTGTGCCAAGGATGGTGTGAG 536
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 Db 121 CTGGGCGCAGAGCCCTCGGTCAAGCCCGCTCTGACTGCGCAAGAAGCACAACCC 180
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 QY 537 CGGTCTCGGTTCCGATGTCAGAGCGGTTGCGTCGGGGCCAGGCCCTACATGTGCAATGA 596
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 Db 181 CATCTCCGACGCCAACGCCGTGAGCGGTTGCAACGGCGGCACCTTCTTACACCTTGCAGCAA 240
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 QY 597 CAACACGACCTGGTGTGTAATGACACCACTTGCTTACGGTTTCGCTGCTGCCAGTCTCGG 656
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 Db 361 CGTGAAGGCGAAGACCATGGTGTGATAGTCCACCAACCGGAGGCGATCTCGGCGAGAA 420
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 QY 1017 CAAGACTGTTGGAGCGCAA 1037
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 Db 652 TCGCACCGGATGCGCGCAA 672

[illegible]

REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED	FEATURES	BASE COUNT	ORIGIN
1	Sheppard, P.O., Grant, F.J., Oort, P.J., Sprecher, C.A., Foster, D.C., Hagen, P.S., Upshall, A., McKnight, G.L. and O'Hara, P.J.	The use of conserved cellulase family-specific sequences to clone cellulase homologue cDNAs from <i>Fusarium oxysporum</i>	Gene 150 (1), 163-167 (1994)	95047531	7959045	Location/Qualifiers 1. .1443 /organism="Fusarium oxysporum" /db_xref="taxon:5507" 83. .1213 /notes="putative" /codon_start=1 /product="K-family cellulase homologue" /protein_id="AAA65589.1" /db_xref="GI:520823" /translations="MRSYVLLALAGPLAVSAASGSHSTRYMDCCPKSCSMGKAAV APALTCDKNDNPISNTNAVNGCGGSAVACTNYSWAVNDELAAYGPAATKISGSEA SWCCACVALTFTTGPVKXKMIQVSTNTGGDLGDNHFDLMPGGGVGIFDGTCTSEBGR ALGGAQYGGISRSSECDSTPELUGDGNRFRWFENADNPDFTEQVQCPKALLDLSG CKRDDSSPFAFGDTSASQPSSSAKKTSAAAAQPOKTKDSAPVQKSTKPA QBPETPAQPKDQKFAVTPAATKPAQVFNKPKTKYKVRGTRGSCPAKTDATATAKA SVVUPYQCGSGSKYAPVNGNLACATSKCKVQKNEYYSQCVPN"	325 a 448 c 332 g 338 t	
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Qy						424 TCTGGAAACGGTCGCACCTACCCGCTACTGGGATGCTGCAAGCCCTCTTGGCGCTGGAC	483	
Db						137 TCTGGAAACGGTCACCTACTTCGATAGTGGGATGCTGCAAGCCCTCTTGGGAGC	196	
Qy						484 GGAAAGCTTCTGTAACTAAGCCTGTACTCACCTGTGCCAAGGATGGTGCAGCCGCTC	543	
Db						197 GGAAAGCTGCTGTCAAGCCCTCTGTTAACTTGTGATAAGAACGCAACCCCATTTCC	256	
Qy						544 GGTTCGAGTTCAGAGCGGTG---CGTCGGCGGCGAGCCCTACATGTGCAATGACAAC	600	
Db						257 AACACCAATGCTGTCAACGGTGTGAGGGTGGTGTCTGCTTATGCTTGCACCAACTAC	316	
Qy						601 CAGCCCTGGTGTCAATGACGACTTGCCTACGTTTGCCTGCTGTCAGCTTCGGTAGC	660	
Db						317 TCTCCCTGGCTGTCAACGATGAGCTTGCCTACGGTTTCCGTGCTACCAAGATCTCGGT	376	
Qy						661 GCCGGTCTCTGCATTCTGCTCGGGCTGTACGAGCTTACCTTCCACCAACCTGCTGC	720	
Db						377 GGCTCCGAGCCAGCTGGTGTCTGTGTCTATGCTTTGACCTTTCACCATGGCCCCGTC	436	
Qy						721 GCTGGCAAGAAGTTTGTGTCAGAGTCACCAACACCGGTGATGATCTCAGCAACCAACAC	780	
Db						437 AAGGCAAGAAGATGATGCTCCAGTCCACCAACTGGAGGTGATCTCGGCGCAACCAAC	496	
Qy						781 TTTGATTTGAGATGCCCGCGGTGTGTGCGGTACTTCAACGGCTGCCAGTCCAGTGG	840	
Db						497 TTGATTCATGATGCCCGCGGTGTGCGGTATCTTTCGACGGCTGCACCTCTGAGT--	554	
Qy						841 AACACCAACCAATGGCTGGGTGCTCGCTATGGCGGTATTAGCTCTATTTTCAGAGTGC	900	
Db						555 -----TCGGCAAGGCTCTCGCGGTGCGCAGTACGGCGGTATCTCTCCCGAAGCGAATGT	610	
Qy						901 GACAAGCTTCTCTACCCAGTGTGCGGTGGTTGCAAGTGGAGATTTCGGATGGTTCAAGAAC	960	
Db						611 GATAGTACCCCGAGCTTCTCAAGACGGTGGCCACTGGCGATTCGACTGGTTCGAGAAC	670	
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Db						671 GCGCAACAACTGACTTCACTTTTGAGCAGGTTCACTGCCCCCAAGGCTCTCTCTCGACATC	730	

[illegible]

Wed Jun 18 17:55:08 2003

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Db 731 AGTGGATGCAAGCG 744

RESULT 5
LOCUS A21795 1473 bp mRNA linear PAT 20-SEP-1995
DEFINITION F. oxysporum mRNA for endonuclease component.
ACCESSION A21795
VERSION A21795.1 GI:1246874
KEYWORDS
SOURCE Fusarium oxysporum.
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
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complex.
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BASE COUNT 343 a 453 c 337 g 340 t
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Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33; Indels 9; Gaps 2;
Matches 392; Conservative 0; Mismatches 213;
QY 424 TCTGGAACCGGTGCGCACTACCGCTACTGGGATTCGTGCAAGCCCTCTTGCGCTGGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATATCGGATTCGTGCAAGCCCTCTTGCTCTTGAGC 210
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QY 544 GGTTCAGATGTCAGAGCGGTG---CGTCGGGGCCAGCGCTACATGTGCAATGACAAC 600
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QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTACGGTTTCGTGCTGCTGCTGCTGCTGCTG 660
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QY 721 GCTGGCAAGAAGTTTCTGCTCCAGGTTCACCAACACCGGTGATGATCTAGCACCAACAC 780
Db 451 AAGGCGCAAGAGATGATGCTCCAGTCCCAACACCTGGAGGTGATCTCGGCGACCAACAC 510
QY 781 TTGATTTGAGATGTCGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 840
Db 511 TTGATTTGAGATGTCGCGCGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 568
QY 841 AACACCAACACGATGCTGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 900
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QY 781 TTTGATTGACAGTCCCGCGGTGTGCTGCTTCAACGGCTGCCAGTCCAGTGG 840
Db 511 TTGATCTCATGATGCCCGGGTGTGCTCGGTATCTTCGAGCTGCACCTCTGAGT-- 568
QY 841 AACACCAACCGATGGGTGCTGCTATGCGGTATGAGCTTATTTAGAGTGC 900
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Db 745 AGTGGATGCAAGCG 758

RESULT 9
A23959
LOCUS A23959 1473 bp DNA linear PAT 01-MAR-1995
DEFINITION Endoglucanase gene.
ACCESSION A23959
VERSION A23959.1 GI:832900
KEYWORDS Fusarium oxysporum.
SOURCE Fusarium oxysporum
ORGANISM Fusarium oxysporum
Eukaryote; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS McCorquodale, F. and Busch, A.
TITLE Dye transfer inhibiting compositions
JOURNAL Patent: EP 0540784-A 3 12-MAY-1993;
THE PROCTER & GAMBLE COMPANY
FEATURES Location/Qualifiers
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QY 424 TCTGGAACCGTCCGACTACCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGAC 483
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Db 211 GGAAGGCTGTCTCAACGCCCTCTTAACTTGTGATAAGAACGACCAACCCATTTC 270
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Db 271 AACACCAATGCTGTCAACCGGTGTGAGGGTGTGCTGTTATGTTGCAACCACTAC 330
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DEFINITION Sequence 3 from Patent EP0633311.
ACCESSION A41660
VERSION A41660.1 GI:2297285
KEYWORDS unidentifed.
SOURCE

ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Herbots, I.M. and Jansen, M.P.
TITLE Hydrophobic amines for cellulase stabilization in liquid detergent compositions containing anionic surfactant and cellulase
JOURNAL Patent: EP 0633311-A 3 11-JAN-1995;
PROCTER & GAMBLE (US)
COMMENT Other publication CA 2165771 950105.
FEATURES
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Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;

QY 424 TCTGGAACCGTTCGCACTACCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGGAC 483
DB 151 TCTGGAACCGTTCCTACTCTACTGATCTGGGATTGCTGCAAGCCCTCTTGGCGCTGGGAC 210
QY 484 GGAAGGCTTCTGTAACTAAGCCTGTACTACCTGTGCCAAGGATGGTGTACGCCGCTTC 543
DB 211 GGAAGGCTTCTGTAACTAAGCCTGTACTACCTGTGCCAAGGATGGTGTACGCCGCTTC 270
QY 544 GGTTCGATGTCAGAGCGGTG---CGTCGGCGGCCAGCCCTACATGTGCAATGACAAC 600
DB 271 AACACCAATGCTGTCAACCGCTGTGAGGGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTTGTCAATGACGACCTTGCTACCGTTTCTGCTGCTGCAAGTCTCGGTAGC 660
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCTACCGTTTCTGCTGCTGCAAGTCTCGGT 390
QY 661 GCCGGTGCCTCTGCATTTCTGCTGCGGCTGTACGAGCTTACCTTCAACCAACATGCTGTC 720
DB 391 GGCTCCGAGCCAGCTGTGCTGTGCTGTGCTATGCTTTGACCTTCAACCACTGCGCCGTC 450
QY 721 GCTGGCAAGATTGCTGCTGCAAGTCCACCAACCGGTGATGATCTCAGCAGCAACCAAC 780
DB 451 AAGGGCAAGAGATGATGCTGCTGCAAGTCCACCAACCGGTGATGATCTCAGCAGCAACCAAC 510
QY 781 TTTGATTGAGATGCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 511 TTGATCTCATGATGCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
QY 841 AACACCAACCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 569 ----TCGGCAAGGCTCTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 901 GACAGCTTCTACCGAGTTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 625 GATAGCTACCCGAGCTTCTCAAGGAGCGTTGCAAGTGGAGATTCGATGCTGCTGCTGCTGCT 684
QY 961 GCTGACAAACCGAGGTCACCTTCAAGGCTGTTACTTGCCTGCGGAGATCATTTGCCAAG 1020
DB 685 GCGGACAAACCTGACTTCACTTTGAGCAGGTTGAGTGGCCCAAGGCTCTCTCTGACATC 744
QY 1021 ACTGGTTGCGAGCG 1034
DB 745 AGTGGATGCAAGCG 758

RESULT 11
AR072922
LOCUS AR072922
DEFINITION Sequence 3 from patent US 5948672.
ACCESSION AR072922
VERSION AR072922.1 GI:9999685
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Rasmussen, G., Mikkelsen, J., Moslashedler, J., Schulein, M., Patkar, S., Anant, H., Hagen, P., Hjort, C., Mailand, and Hastrup, S.
TITLE Cellulase preparation comprising an endoglucanase enzyme
JOURNAL Patent: US 5948672-A 3 07-SEP-1999;
FEATURES
source Location/Qualifiers
1. .1473
/organism="unknown"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;

QY 424 TCTGGAACCGTTCGCACTACCGCTACTGGGATTGCTGCAAGCCCTCTTGGCGCTGGGAC 483
DB 151 TCTGGAACCGTTCCTACTCTACTGATCTGGGATTGCTGCAAGCCCTCTTGGCGCTGGGAC 210
QY 484 GGAAGGCTTCTGTAACTAAGCCTGTACTACCTGTGCCAAGGATGGTGTACGCCGCTTC 543
DB 211 GGAAGGCTTCTGTAACTAAGCCTGTACTACCTGTGCCAAGGATGGTGTACGCCGCTTC 270
QY 544 GGTTCGATGTCAGAGCGGTG---CGTCGGCGGCCAGCCCTACATGTGCAATGACAAC 600
DB 271 AACACCAATGCTGTCAACCGCTGTGAGGGTGGTGTCTGCTTATGCTTGCAACCACTAC 330
QY 601 CAGCCCTGGGTTGTCAATGACGACCTTGCTACCGTTTCTGCTGCTGCAAGTCTCGGTAGC 660
DB 331 TCTCCCTGGGCTGTCAACGATGAGCTTGCTACCGTTTCTGCTGCTGCAAGTCTCGGT 390
QY 661 GCCGGTGCCTCTGCATTTCTGCTGCGGCTGTACGAGCTTACCTTCAACCAACATGCTGTC 720
DB 391 GGCTCCGAGCCAGCTGTGCTGTGCTGTGCTATGCTTTGACCTTCAACCACTGCGCCGTC 450
QY 721 GCTGGCAAGATTGCTGCTGCAAGTCCACCAACCGGTGATGATCTCAGCAGCAACCAAC 780
DB 451 AAGGGCAAGAGATGATGCTGCTGCAAGTCCACCAACCGGTGATGATCTCAGCAGCAACCAAC 510
QY 781 TTTGATTGAGATGCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
DB 511 TTGATCTCATGATGCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568
QY 841 AACACCAACCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
DB 569 ----TCGGCAAGGCTCTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 901 GACAGCTTCTACCGAGTTCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 625 GATAGCTACCCGAGCTTCTCAAGGAGCGTTGCAAGTGGAGATTCGATGCTGCTGCTGCTGCT 684
QY 961 GCTGACAAACCGAGGTCACCTTCAAGGCTGTTACTTGCCTGCGGAGATCATTTGCCAAG 1020
DB 685 GCGGACAAACCTGACTTCACTTTGAGCAGGTTGAGTGGCCCAAGGCTCTCTCTGACATC 744
QY 1021 ACTGGTTGCGAGCG 1034
DB 745 AGTGGATGCAAGCG 758

RESULT 12
BD002249
LOCUS BD002249
DEFINITION Cellulase preparation comprising endoglucanase.
ACCESSION BD002249
VERSION BD002249.1 GI:18630210
KEYWORDS JP 2000217583-A/2.
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum.
Hypocreales; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum

complex.
1 (bases 1 to 1473)
REFERENCE Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S.
AUTHORS Gurete,R., Moller,M.J., Martin,S. and Ananto,P.S.
TITLE Cellulase preparation comprising endoglucanase
JOURNAL Patent: JP 2000217583-A 2 08-AUG-2000;
COMMENT OS Fusarium oxysporum
NOVO NORDISK A/S
PN JP 2000217583-A/2
PD 08-AUG-2000
PF 22-DEC-1999 JP 1999365341
PR 09-MAY-1990 DK 1159/90,22-APR-1991 DK 0736/91 PI
RASMUSSEN GURETE,MIKKJELSEN JAN MOLLER,SCHREIN MARTIN, PI PATKUL
SHAMKANTO ANANTO
PC C12N15/09,C11D3/386,C12N1/15,C12N1/19,C12N9/42,C12N3/04, PC
D06M16/00//
PC D21H11/20, (C12N9/42,C12R1:645),C12N15/00
CC
FH Key Location/Qualifiers
FT CDS (97). .(1224).
FEATURES
source Location/Qualifiers
1. .1473
/organism="Fusarium oxysporum"
/db_xref="taxon:5507"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No.1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAAACGGTCGACATACCCGCTACTGGGATTGTCGCAAGCCCTCTTGGCGCTGGGAC 483
Db 151 TCTGGAAACGGTCGACATACCCGCTACTCGATATCTGGGATTGTCGCAAGCCCTCTTGGCGCTGGGAC 210
QY 484 GGAAGGCTTCTGTAACCTGCTACTACCTGTCGCAAGGATGCTGACCGCTCTC 543
Db 211 GGAAGGCTTCTGTAACCTGCTACTACCTGTCGCAAGGATGCTGACCGCTCTC 270
QY 544 GGTTCGATGTCAGAGCGGTG---CGTCGGCGCCAGGCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTTATGCTTGCACCAACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTACGGTTTGGTGTGCTGCTGCGATCTCGGTAGC 660
Db 331 TCTCCCTGGGTGTCAACGATGACCTTGCCTACGGTTTGGTGTGCTGCTGCTGCTGCTGCT 390
QY 661 GCCGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 391 GGCTCCGAGGCGACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
QY 721 GCTGGCAAGAGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 451 AAGGCAAGAGATGATGCTCCAGTCCACCAACTGGAGTGATCTCGGCGACCAACCAC 510
QY 781 TTTGATTTGCAAGTCCCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 511 TTGATCTCATGATGCTCCCGGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568-
QY 841 AACACCAACACCGATGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 901 GACAAGCTTCTACCGAGTTCGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 625 GATAGCTACCCCGAGCTTCTCAAGGAGCGTGGTGGCACTGGGAGTTCGACTGGTTCGAGAAC 684
QY 961 GCTCACAAACCCAGAGGTACCTTCAAGCTGCTTACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 685 GCCGACAAACCTGACTTCACTTTGACAGAGTTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
QY 1021 ACTGGTTCGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

RESULT 13
LOCUS BD010853 1473 bp DNA linear PAT 31-JAN-2002
DEFINITION Cellulase preparation containing endoglucanase.
ACCESSION BD010853
VERSION BD010853.1 GI:18639226
KEYWORDS JP 2001057894-A/2.
SOURCE Fusarium oxysporum.
ORGANISM Fusarium oxysporum
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; mitosporic Hypocreales; Fusarium; Fusarium oxysporum
complex.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Rasmussen,G., Mikkelsen,J.M., Schilein,M., Patkar,S.A., Hagen,F.,
Miland,H.K. and Hallstøp,S.
TITLE Cellulase preparation containing endoglucanase
JOURNAL Patent: JP 2001057894-A 2 06-MAR-2001;
COMMENT NOVO NORDISK AS
OS Fusarium oxysporum
PN JP 2001057894-A/2
PD 06-MAR-2001
PF 06-JUL-2000 JP 2000205757
PR 09-MAY-1990 DK 1159/90,22-APR-1991 DK 0736/91 PI
GURETE RASMUSSEN, JAN MOLLER MIKKJELSEN, MARTIN SCHILEIN, PI
SHAMKANT ANANT PATKAR, FRED HAGEN, HJORT KARSTEN MILAND, PI SVEND
HALLSTØP
PC C12N15/09,C11D3/386,C12N1/15,C12N1/19,C12N9/24,D06M16/00// PC
(C12N15/09,C12R1:77), (C12N15/09,C12R1:645), (C12N9/24, PC
C12R1:865),
PC (C12N9/24,C12R1:885), (C12N9/24,C12R1:78), (C12N15/00,C12R1:69),
PC (C12N9/24,C12R1:685), (C12N15/00,C12N15/00,C12R1:77),
(C12N15/00, PC C12R1:645)
CC
FH Key Location/Qualifiers
FT CDS 97. .1224.
FEATURES
source Location/Qualifiers
1. .1473
/organism="Fusarium oxysporum"
/db_xref="taxon:5507"
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN
Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No.1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
QY 424 TCTGGAAACGGTCGACATACCCGCTACTGGGATTGTCGCAAGCCCTCTTGGCGCTGGGAC 483
Db 151 TCTGGAAACGGTCGACATACCCGCTACTCGATATCTGGGATTGTCGCAAGCCCTCTTGGCGCTGGGAC 210
QY 484 GGAAGGCTTCTGTAACCTGCTACTACCTGTCGCAAGGATGCTGACCGCTCTC 543
Db 211 GGAAGGCTTCTGTAACCTGCTACTACCTGTCGCAAGGATGCTGACCGCTCTC 270
QY 544 GGTTCGATGTCAGAGCGGTG---CGTCGGCGCCAGGCTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTGTGAGGGTGTGCTGCTTATGCTTGCACCAACTAC 330
QY 601 CAGCCCTGGGTGTCAATGACGACCTTGCCTACGGTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 331 TCTCCCTGGGTGTCAACGATGACCTTGCCTACGGTTTGGTGTGCTGCTGCTGCTGCTGCTGCTGCT 390
QY 661 GCCGGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 391 GGCTCCGAGGCGACCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
QY 721 GCTGGCAAGAGTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 451 AAGGCAAGAGATGATGCTCCAGTCCACCAACTGGAGTGATCTCGGCGACCAACCAC 510
QY 781 TTTGATTTGCAAGTCCCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840
Db 511 TTGATCTCATGATGCTCCCGGGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 568-
QY 841 AACACCAACACCGATGGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 624
QY 901 GACAAGCTTCTACCGAGTTCGAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 625 GATAGCTACCCCGAGCTTCTCAAGGAGCGTGGTGGCACTGGGAGTTCGACTGGTTCGAGAAC 684
QY 961 GCTCACAAACCCAGAGGTACCTTCAAGCTGCTTACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
Db 685 GCCGACAAACCTGACTTCACTTTGACAGAGTTGAGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
QY 1021 ACTGGTTCGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

Db 511 TTGGATCTCATGATGCCCGCGGTGGTTCGGTATCTTCGACGGCTGCACCTCTGAGT-- 568
Qy 841 AACACCAACACCATGGCTGGGTGCTCGTATGCGGTATTTAGCTCTATTTCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTACGGCGGTATCTCTCTCCGACGGAATGT 624
Qy 901 GACAAGCTTCTTACCCAGTTCGAGGCTGGTTCGAAGTGGAGATTCGGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTTCGACTGGTTCCGAGAAC 684
Qy 961 GCTGACAAACCCAGAGTCACTTCAAGGCTGTTACTTGGCCCTGCCGAGATCATTTGCCAAG 1020
Db 685 GCGGACAAACCTTCACTTTGAGCAGGTTCAAGTGGCCCAAGGCTCTCTCTCGACATC 744
Qy 1021 ACTGGTTGGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

RESULT 14
LOCUS I13885 1473 bp DNA linear PAT 26-SBP-1995
DEFINITION Sequence β from patent US 5443750.
ACCESSION I13885
VERSION I13885.1 GI:996365
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Convents, A., Busch, A. and Baeck, A.C.
TITLE Detergent compositions with high activity cellulase and softening
JOURNAL Patent: US 5443750-A 3 22-AUG-1995;
FEATURES Location/Qualifiers
source 1..1473
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
Qy 424 TCTGGAACGGTCGCACTACCGCTACTCGGATGCTGCAAGCCCTTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATACGGGATGCTGCAAGCCCTTTCTTGGCTTTGGAGC 210
Qy 484 GGAAGGCTTCTGTAAGCTTACTCACCTGTGCCAAGGATGGTGCAGCCGCTC 543
Db 211 GGAAGGCTGCTGTCAAGCCCTGCTTTAACTTGTGATGAAGAACACCAACCATTTCC 270
Qy 544 GGTTCGATGTCCAGAGCGGTG---CGTCGGCGCCAGCGCTTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTGCTTATGCTTGCACCAACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCCTACGGTTTCGCTGCTGCCAGTCTCGGTAGC 660
Db 271 AACACCAATGCTGTCAAGCGTTGTGAGGGTGGTGTCTGCTTATGCTTGCACCAACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCCTACGGTTTCGCTGCTGCCAGTCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGTTCGCTACGAGTTTTCGCTGCTTACCAAGATCTCCGGT 390
Qy 661 GCGGGTGCCTCTGCTGCTGCGGTGTTACGAGCTTACCTTACCAACACTGCTGTC 720
Db 391 GGTTCGAGCCAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
Qy 721 GCTGGAAGAAGTTTGTGCTCAAGTCAACCAACCGGTGATGATCTCAGACCAACAC 780
Db 451 AAGGGCAAGAAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGCAACAC 510
Qy 781 TTTGATTTGAGATGCCCGCGGTGGTGTCCGCTACTTCAACGGCTGCCAGTCTCCAGTGG 840
Db 511 TTGGATCTCATGATGCCCGCGGTGGTGTCCGATCTCTTCGACGGCTGCACCTCTGAGT-- 568

Qy 841 AACACCAACACCGATGGCTGGGTGCTCGTATGCGGTATTTAGCTCTATTTCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTACGGCGGTATCTCTCTCCGACGGAATGT 624
Qy 901 GACAAGCTTCTTACCCAGTTCGAGGCTGGTTCGAAGTGGAGATTCGGATGGTTCAAGAAC 960
Db 625 GATAGCTACCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTTCGACTGGTTCCGAGAAC 684
Qy 961 GCTGACAAACCCAGAGTCACTTCAAGGCTGTTACTTGGCCCTGCCGAGATCATTTGCCAAG 1020
Db 685 GCGGACAAACCTTCACTTTGAGCAGGTTCAAGTGGCCCAAGGCTCTCTCTCGACATC 744
Qy 1021 ACTGGTTGGAGCG 1034
Db 745 AGTGGATGCAAGCG 758

RESULT 15
LOCUS I21317 1473 bp DNA linear PAT 07-OCT-1996
DEFINITION Sequence 3 from patent US 5520838.
ACCESSION I21317
VERSION I21317.1 GI:1601671
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1473)
AUTHORS Baeck, A.C., Ceulemans, R.A. and Busch, A.
TITLE Compact detergent compositions with high activity cellulase
JOURNAL Patent: US 5520838-A 3 28-MAY-1996;
FEATURES Location/Qualifiers
source 1..1473
BASE COUNT 343 a 453 c 337 g 340 t
ORIGIN

Query Match 22.6%; Score 235.2; DB 6; Length 1473;
Best Local Similarity 63.8%; Pred. No. 1e-33;
Matches 392; Conservative 0; Mismatches 213; Indels 9; Gaps 2;
Qy 424 TCTGGAACGGTCGCACTACCGCTACTCGGATGCTGCAAGCCCTTTGGCGCTGGAC 483
Db 151 TCTGGAAGCGGTCACTCTACTCGATACGGGATGCTGCAAGCCCTTTCTTGGCTTTGGAGC 210
Qy 484 GGAAGGCTTCTGTAAGCTTACTCACCTGTGCCAAGGATGGTGCAGCCGCTC 543
Db 211 GGAAGGCTGCTGTCAAGCCCTGCTTTAACTTGTGATGAAGAACACCAACCATTTCC 270
Qy 544 GGTTCGATGTCCAGAGCGGTG---CGTCGGCGCCAGCGCTTACATGTGCAATGACAAC 600
Db 271 AACACCAATGCTGTCAACGGTTGTGAGGGTGGTGTCTGCTTATGCTTGCACCAACTAC 330
Qy 601 CAGCCCTGGGTTGTCAATGACGACCTTGCCTACGGTTTCGCTGCTGCCAGTCTCGGTAGC 660
Db 331 TCTCCCTGGGCTGTCAACGATGAGTTCGCTACGAGTTTTCGCTGCTTACCAAGATCTCCGGT 390
Qy 661 GCGGGTGCCTCTGCTGCTGCGGTGTTACGAGCTTACCTTACCAACACTGCTGTC 720
Db 391 GGTTCGAGCCAGCTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 450
Qy 721 GCTGGAAGAAGTTTGTGCTCAAGTCAACCAACCGGTGATGATCTCAGACCAACAC 780
Db 451 AAGGGCAAGAAGATGATGCTCCAGTCCACCAACACTGGAGGTGATCTCGGCGCAACAC 510
Qy 781 TTTGATTTGAGATGCCCGCGGTGGTGTCCGCTACTTCAACGGCTGCCAGTCTCCAGTGG 840
Db 511 TTGGATCTCATGATGCCCGCGGTGGTGTCCGATCTCTTCGACGGCTGCACCTCTGAGT-- 568
Qy 841 AACACCAACACCGATGGCTGGGTGCTCGCTATGCGGTATTTAGCTCTATTTCAGAGTGC 900
Db 569 ----TCGGCAAGGCTCTCGCGGTGCCAGTACGGCGGTATCTCTCTCCGACGGAATGT 624

Qy	901	GACAAGCTTCCTACCCAGTTGCAAGGTGGTTGCAAGTGGAGATTGCGATGGTTCAAGAAC	960
Db	625	GATAGCTACCCCGAGCTTCTCAAGGACGGTTGCCACTGGCGATTGCACTGGTTGCGAGAAC	684
Qy	961	GCTGACAAACCCAGAGGTCACTTCAAGGCTGTACTTGGCCCTGCCGAGATCATTTGCCAAG	1020
Db	685	GCCGACAACCCCTGACTTCACTTTGAGCAGGTTTCAGTGCCCCCAAGGCTCTCTCGACATC	744
Qy	1021	ACTGGTTGCGAGCG	1034
Db	745	AGTGGATGCAAGCG	758

Search completed: June 17, 2003, 16:24:55
 Job time : 2682.05 secs